

Percent Similarity: 98.001 Percent Identity: 98.001

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DEFINITION Rattus norvegicus SynGAP-b mRNA, complete cds.
ACCESSION AF058790

VERSION AF058790.1 GI:3722228
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4140)
AUTHORS Kim, J.H., Liao, D., Lau, L.F. and Haganir, R.L.
TITLE SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90
protein family
JOURNAL Neuron 20 (4), 683-691 (1998)
MEDLINE 98240917
REFERENCE 2 (bases 1 to 4140)
AUTHORS Kim, J.H. and Haganir, R.L.
TITLE Direct Submission
JOURNAL Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical
Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
REFERENCE 3 (bases 1 to 4140)
AUTHORS Kim, J.H. and Haganir, R.L.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1998) Neuroscience, Johns Hopkins Medical
Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
REMARK Sequence update by submitter
COMMENT On Oct 9, 1998 this sequence version replaced gi:3065890.
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Align seg 1/1 to: AF058790 from: 1 to: 4140

98.7%

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TITLE	SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family	
JOURNAL	Neuron 20 (43), 683-691 (1998)	
MEDLINE	98240917	
REFERENCE	2 (bases 1 to 4265)	
AUTHORS	Kim,J.H. and Huganir,R.L.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-FEB-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCRB 900, Baltimore, MD 21205, U.S.A.	
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CDS

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DEFINITION Rattus norvegicus synaptic ras GTPase-activating protein p135

ACCESSION AF048976

VERSION AF048976

KEYWORDS

SOURCE

ORGANISM

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 4063)

Chen, H.-J. and Kennedy, M.B.

Identification and cloning of a novel 130 kd protein containing a

ras GTPase-activating domain from the rat forebrain postsynaptic

density

(Int) SOC. NEUROSCI. ABSTR.: 1466; (1997)

2 (bases 1 to 4063)

Chen, H.-J., Rojas-Soto, M. and Kennedy, M.B.

A synaptic ras GTPase-activating protein (p135 SynGAP) inhibited by

Cam kinase II

Unpublished

3 (bases 1 to 4063)

Chen, H.-J. and Kennedy, M.B.

Direct Submission

Submitted (17-FEB-1998) Division of Biology, California Institute

of Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA

91125, USA

location/Qualifiers

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123..4003

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Beckhandale

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FEATURES

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 AUTHORS Suzuki, T.
 TITLE SynGAP-d
 JOURNAL Published Only in DataBase (1999) In press
 REFERENCE 2 (bases 1 to 4801)
 AUTHORS Suzuki, T.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo Suzuki, Shinshu University School of Medicine, Department of Neuroplasticity, 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan (E-mail:suzukit@sch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683, Fax:+81-263-37-2725)
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VERSION    AL161903.12 GI:10039702
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SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Tracey A.
            Direct Submission
            Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
            requests: clonerques@sanger.ac.uk
            On Sep 9, 2000 this sequence version replaced gi:9796876.
            ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquerry@sanger.ac.uk
            ----- Project Information
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            Center project name: BAI75A4

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----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 145680 bases at least Q40
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Insert size: 150756; sum-of-contigs
Quality coverage: 6.43x in Q20 bases; agarose-fp
coverage: 6.54x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 54611: contig of 54611 bp in length
* 54612 54711: gap of 100 bp
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FEATURES

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Fri Jan 19 08:02:58 2001

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Date: Jan 19, 2001 7:43 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+gln.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09294298/runat_17012001_125501_27768/app_query.fasta_1.4359
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Search information block:

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Query length: 1423
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; Patent No. 5760203
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; APPLICANT: Wong, Gail L.
; APPLICANT: Martin, George
; APPLICANT: McCormick, Francis P.
; APPLICANT: Rubinfeld, Bonnie
; APPLICANT: O'Rourke, Edward C.
; APPLICANT: Clark, Robin
; TITLE OF INVENTION: GAP Gene Sequences
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,687B
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/774,644
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/260,807
; FILING DATE: 21-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/230,761
; FILING DATE: 10-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27527/31898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100...2709
; US-08-190-687B-24

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1406 ATCCATATTGTAACATCTACCTGATAGTGTCCAAAGTAGCAAAACATCAT 1455
281 SerLysProArgSerAlaSerGlyAspThrValPheTrpGlyGluHisph 297
: : : : : : : : : : : : : : : : : : : : : : : : :
1456 GCAAGG.....GAAGGCCAAACCCAGTATGGTCAGAGAGTT 1493
297 eGluPheAsnAsnLeuProAla...ValArgAlaLeuArgLeuHisLeu 313
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1494 TGCTTTGATGATCTCTCTCGACATCAATAGATTGAAATACTCTT. 1542
313 yArgAspSerAspLysLysArgLysLysAspLysAlaGlyTyValGly 329
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330 LeuValThrValProValAlaThrLeuAlaGlyArgHisPheThrGlu 346
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346 nTrpTrpProValThr.....LeuProThrGlySerGlyGlySerGly 361
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1632 ATGGTTTCTGTCAGCTCCCATATACCAATTA..... 1662
361 LyMetGlySerGlyGlyGlyGlyGlySerGlyGlySerGlyGlyLys 377
1662 ..... 1662
378 GlyLysGlyGlyCysPro...AlaValArgLeuLysAlaArgTyGlnTh 393
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1663 ...AAAGGTATTGAACACGAGGTCCTCGGTGTTCCAGCAGCATACTCTAT 1709
393 rMetSerIleLeuProMetGluLeuTyLysLysPheAlaGluTyVal 410
: : : : : : : : : : : : : : : : : : : : : : : : :
1710 GGAARAAATCATGCCAAGAGAGTAGTCAGTGAATTTAAGAGCTTATAC 1759
410 hrAsnHisTyArgMetLeuCysAlaValLeuGluProAlaLeuAsnVal 426
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1760 TCAAAAAGGAAGTTCATGCTAGTCTATGCTTTATCA.....CATGTA 1800
427 LysGlyLysGluGlu.....ValAlaSerAlaLeuValHisIleLeu 441
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1801 TGTGACACAGACCGAACACTACTGCCAGCATCTCTACTGAGGATTTCT 1850
441 nSerThrGlyLysAlaLysAspPheLeuSerAspMetAlaMetSerGlu 458
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1851 TCACGAAAGAGCTTGAATCGTTGTTGTTATGCACACTAAATGCACAGAAA 1900
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1901 TAAGC.....ATGGAAGATGAAGCCACTACCTATTTTCGAGCCCAACA 1944
474 LeuAlaThrLysAlaIleGluGluTyMetArgLeuIleGlyGlnLysTy 490
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1945 CTTCAAGCACCTTGATGGAGCAGTATATGAAAGCCACTGCTACACAGTT 1994
490 rLeuLysAspAlaIleGlyGluPheIleArgAlaLeuTyGluSerGlu 507
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1995 TGTTCATCATGCTTTGAAAGACTCTATTTTAAAGATAATGGAAGCAAGC 2044
507 luAsnCysGluValAspProIleLysCysThrAlaSerSerLeuAlaGlu 523
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524 HisGlnAlaAsn.....LeuArgMetCysCysGluLeuAlaLeuCys 538
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538 sValValAsnSerHisCysValPheProArgGluLeuLysGluValPhe 555
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598 luTyProAspGluGlnThrSerArgThrLeuThrLeuAlaLysVal 614
: : : : : : : : : : : : : : : : : : : : : : : : :
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615 IleGlnAsnLeuAlaAsnPheSerLysPheThrSerLysGluAspPhe 631
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665 GluGlyTyTrpIleAspLeuGlyArgGluLeuSerThrLeuHisAlaLe 681
: : : : : : : : : : : : : : : : : : : : : : : : :
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681 u.....TrpGluValLeuProGlnLeuSerLysGlu..... 691
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692 .....AlaLeuLysLeuGlyProLeuProArgLeuLeuSerAsp 705
: : : : : : : : : : : : : : : : : : : : : : : : :
2624 AGCAGCAGCTATTGAAAAGCTTCTGGCTATAACAGAACTGCTTCAACA 2673
706 IleSerThrAlaLeuArgAsnProAsn...IleGlnArgGlnProSer 721
: : : : : : : : : : : : : : : : : : : : : : : : :
2674 AAACAAACCATGATACAAAAACCAATGATGTCCAGGTAGCGCTTCGCC 2723
721 gGln 722
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2724 CCAG 2727

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-190-687B-7

seq_documentation_block:

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ID56/gcgdata/geneseq/NA1991	DAT	Q10988	+	435.50	304.14	3.7e-09
ID56/gcgdata/geneseq/NA1997	DAT	Q176739	+	429.50	303.57	4.0e-09
ID56/gcgdata/geneseq/NA1998	DAT	V621676	+	310.00	191.75	0.0068
ID56/gcgdata/geneseq/NA2000	DAT	V628130	+	309.00	205.94	0.0011
ID56/gcgdata/geneseq/NA2007	DAT	V628715	+	304.00	202.45	0.0017
ID56/gcgdata/geneseq/NA2009	DAT	V258980	+	295.50	201.64	0.0013
ID56/gcgdata/geneseq/NA2000	DAT	V234430	+	283.00	197.52	0.0033
ID56/gcgdata/geneseq/NA1995	DAT	V6286927	+	273.00	189.44	0.0092
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ID56/gcgdata/geneseq/NA1999	DAT	V56436	+	260.50	181.24	0.0263
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ID56/gcgdata/geneseq/NA1997	DAT	T87508	-	256.00	161.21	0.3428
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ID56/gcgdata/geneseq/NA1999	DAT	V36583	+	253.50	172.30	0.0827
ID56/gcgdata/geneseq/NA1992	DAT	Q29263	+	253.00	174.75	0.0640
ID56/gcgdata/geneseq/NA1996	DAT	Q6978	+	252.00	177.05	0.0450
ID56/gcgdata/geneseq/NA1995	DAT	V21373	+	252.00	177.05	0.0450
ID56/gcgdata/geneseq/NA1998	DAT	V62134	+	252.00	162.30	0.2982
ID56/gcgdata/geneseq/NA1999	DAT	V62148	+	251.50	175.18	0.0372
ID56/gcgdata/geneseq/NA1995	DAT	Q80016	+	251.00	185.85	0.0145
ID56/gcgdata/geneseq/NA1992	DAT	Q20602	+	251.00	169.65	0.1162
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ID56/gcgdata/geneseq/NA1997	DAT	Q6704	+	250.00	176.72	0.0469
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ID56/gcgdata/geneseq/NA1994	DAT	Q73500	+	247.50	167.63	0.1506
ID56/gcgdata/geneseq/NA1995	DAT	Q84659	+	247.00	167.86	0.1462
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ID56/gcgdata/geneseq/NA1993	DAT	Q50631	+	245.00	174.01	0.0664
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ID56/gcgdata/geneseq/NA1994	DAT	Q64201	+	244.00	168.51	0.1344
ID56/gcgdata/geneseq/NA1994	DAT	Q53954	+	243.00	171.65	0.0899
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ID56/gcgdata/geneseq/NA1996	DAT	T17420	+	242.50	174.45	0.0628
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194 VALTHSERST
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194 vaTHISserTIELEuGLYngIGfneCysfneGruvaIMr
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210 rSerGlyThrLys.....CysPheAlaCysArgSerAlaA 222
1756 GCACCTTAGTGAGACACATACATCTTTTACCTTTCGACGAGAACTCCAG 1805
222 lagluArgAspLysTrpIleGluAsnLeuGln.....Arg 233
1806 AACAAAGCAGAGGATTGGATGAAGGTCTCAGGCGATTTTGCATTTACGG 1855
234 AlaValLysProAsnLysAspAsnSerArg...ArgValAspAsnValLe 249
1856 AAAAGTAGTCCAGGACATCCCAATAAACCCCTTCGTACGTCGCGCGCT 1905
249 uLysLeuTrpIleIleGluAlaArgGluLeuProLys.....LysA 264
1906 TGTTTACATATTGAAGAAGCCCATAACTCCAGTAAACATTTTACTA 1955
264 rGlyTrpCysGluLeuLysLeuAspMetLeuTyAlaArgThrThr 280
1956 ATCCATATTGTAACATCTACCTGAATAGTCTCAAGTAGCAAAACTCAT 2005
281 SerLysProArgSerAlaSerGlyAspThrValPheTrpGlyGluHisPh 297
2006 GCAAGG.....GAAGGCCAAACCCAGTAGTGTGTCAGAAGGTT 2043
297 eGluPheAsnAsnLeuProAla...ValArgAlaLeuArgLeuHisLeu 313
2044 TGCTTTGATGATCTTCCCTGACATCAATAGATTGAAATAACTCTT. 2092
313 yrArgAspSerLysLysArgLysAspLysAlaGlyTrpValGly 329
2093 .....ACTAATAAACAAAGAAAGCAAGATCCTCATATCTTA 2131
330 LeuValThrValProValAlaThrLeuAlaGlyArgHisPheThrGluG 346
2132 TTTATGCGCTGCCAGTGGCCGATTACAGAAAGGCCATGCCACAGATGA 2181
346 nTrpTrpProValThr.....LeuProThrGlySerGlyGlySerGlyG 361
2182 ATGTTTCTGCTCAGCTCCCATATACCATTA..... 2212
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2212 ..... 2212
378 GlyLysGlyGlyCysPro...AlaValArgLeuLysAlaArgTrpGlnTh 393
2213 ...AAGGTATTGAACACGAGGTCCTGCTGTTCGAGCAGCATCTCTAT 2259
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2260 GGAATAATCATGCCAGAGAGAGTACAGTGAATTTAAAGAGCTTATAC 2309
410 hrAsnHisTrpArgMetLeuCysAlaValLeuGluProAlaLeuAsnVal 426
2310 TGCAAAAGGACTTCATGTAGTCTATGCTTTATCA.....CATGTA 2350
427 LysGlyLysGluGlu.....ValAlaSerAlaLeuValHisIleLeuGl 441
2351 TGTGGACAGACCGACACTACTGTCGACGATCCTACTGAGGATTTTCT 2400
441 nSerThrGlyLysAlaLysAspPheLeuSerAspMetAlaMetSerGluV 458
2401 TCAGAAAGCTTGAATGTTGTTGTATGCACACTAATGACAGAGAA 2450
458 alaAspArgPheMetGluArgGlu...HisLeuIlePheArgGluAsnThr 473
2451 TAAGC.....ATGGAAGATGAGGACCACTACCCCTATTTTCGAGCCACA 2494
47 LeuAlaThrLysAlaIleGluGluTrpMetArgLeuIleGlnLysTy 490
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seq_name: /SID56/gcdata/geneseq/geneseq/NA1991.DAT.Q10988

seq_documentation_block:

ID Q10988 standard; cDNA; 4307 BP.

XX Q10988;

XX AC

DT 22-MAY-1991 (first entry)

OM of: US-09-294-298-2 to: EST:* out_format : pfs

Date: Jan 18, 2001 9:24 PM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2.1/USPTO_spool/US09294298/runat_17012001.125501.27745/app_query.fasta_1.4359
-DB=EST -QFWT=fastap -SUFFIX=rst -CAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELETE=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFWT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09294298 @CGNL1_17119 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-294-298-2

Query length: 1423

Database: EST:*

Database sequences: 7991742

Database length: -791223438

Search time (sec): 4688.750000

score_list:

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gb_gss21:AA399131	-	764.00	879.28	5.8e-40	474	AZ399131 IM0164P14R Mouse 10kb
gb_est49:AW79747	-	737.50	846.16	4.0e-38	593	AW79747 hn85f10.x1 NCI_CGAP_K1
gb_est44:AW421227	-	731.50	839.16	9.9e-38	597	AW421227 fj94f10.x1 zebrafish 9
gb_est71:BA490923	+	706.00	809.16	4.6e-36	628	BE490923 db38g08.x1 Blackspear
gb_est22:AI606711	+	660.00	757.27	3.6e-33	566	AI606711 ml58d01.y1 Stratagene
gb_est71:BA63433	+	628.50	723.22	2.8e-31	463	BE63433 hw23d06.x1 NCI_CGAP_K1
gb_est22:AI57567	-	600.00	689.22	2.2e-29	511	AI57567 UI-R-Y0-vk-d-04-0-UI.s
gb_est41:AW205989	+	571.50	657.19	1.4e-27	474	AW205989 UI-H-B11-afv-d-12-0-UI
gb_est28:AJ396547	+	566.50	646.86	5.1e-27	707	AJ396547 AJ396547 dkf2426 Gallu
gb_est11:AA709010	-	563.00	638.57	4.1e-27	427	AA709010 zf94h11.s1 Soares_pine
gb_est22:AI609604	-	548.50	631.00	3.9e-26	460	AI609604 tw91e09.x1 NCI_CGAP_K1
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gb_est74:BB695648	+	484.50	559.37	3.8e-22	379	AA575948 nm56e05.s1 NCI_CGAP_B
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gb_est39:AW076911	+	480.00	552.47	9.2e-22	440	AA107246 ml58d01.s1 Stratagene
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gb_gss27:CN504DL0	+	416.50	471.35	3.0e-17	877	AL285885 Tetraodon nigroviridis
gb_est4:AA258366	-	401.50	465.57	6.4e-17	319	AA258366 zt59e01.s1 Soares_Nhm
gb_gss27:CN504LW	+	401.00	452.85	3.3e-16	926	AL270761 Tetraodon nigroviridis
gb_est47:BB394547	+	394.00	450.88	4.2e-16	542	AW56799 109245 MARC lBOV Bos t
gb_est61:BB394547	+	383.50	444.59	9.4e-16	325	BB394547 BB394547 RIKEN full-le
gb_est23:AI650331	+	379.00	440.47	1.6e-15	296	AI650331 wal8f01.x1 NCI_CGAP_K1
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gb_est59:BB312776 + 365.50 424.40 1.3e-14 309 + BB312776 BB312776 RIKEN full
gb_est75:BE773015 - 365.50 419.36 2.4e-14 481 + BE773015 K1-FT0134-170700-0
gb_est19:AI327335 - 358.00 407.25 1.1e-13 651 + AI327335 mp74c11.x1 Soares_t
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seq_name: gb_est37:AV590698

seq_documentation_block: 571 bp mRNA EST 29-AUG-2000
LOCUS AV590698 Bos taurus brain fetus Bos taurus cDNA clone E1BR014B04
DEFINITION AV590698 Bos taurus brain fetus Bos taurus cDNA clone E1BR014B04
5', mRNA sequence.

ACCESSION AV590698
VERSION AV590698.1 GI:9701691
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 571)
AUTHORS Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
Suzuki,H.

TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division

Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725

Email: kazusugi@ccoc.acn.ne.jp

Single pass sequencing

This clone was obtained from a polyA-deleted cDNA library.

FEATURES
source

1..571
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1BR014B04"
/clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
/dev_stage="fetus"
/lab_note="DH10B"
/host="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 124 a 161 c 169 g 116 t
ORIGIN

alignment_scores:

Quality: 933.00 Length: 186
Ratio: 5.043 Gaps: 1
Percent Similarity: 99.462 Percent Identity: 99.462

alignment_block:

US-09-294-298-2 x AV590698

Align seg 1/1 to: AV590698 from: 1 to: 571

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13 AAGAGGAGGTCGGCAGTGCTCTGTTTCACATCTCGAGAGTACAGGCAA 62
445 sAlaLysAspPheLeuSerAspMetAlaMetSerGluValAspArgPheM 462
63 GGCCAAGGACCTCTCTTTCAGACATGGCCATCTCCGAGGTGGACGGTTCA 112
462 etGluArgGluHisLeuIlePheArgGluAsnThrLeuAlaThrLysAla 478
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113 TGGACGAGAGAACCTCATATATCCGCGAGAACGCTCGCCACTAAAGGCC 162
479 IleGluGluTyrMetArgLeuIleGlyGlnLysTyrLeuLysAspAlaIle 495
163 ATAGAAGAGTACATGAGACTGATTGGTCAGAAATACCTCAGAGTGCAT 212

495 eGlyGluPheIleArgAlaLeuTyrGluSerGluGluAsnCysGluVala 512
 213 CGGGAAATTCATCGTCTGTATGAATCTGAGGAGAACTGTGAGGTGG 262
 512 spProlLeuLysCysThrAlaSerSerLeuAlaGluHisGlnAlaAsnLeu 528
 263 ACCCCATCAAGTACAGGATCCAGTTTGGCTGAGCACCAGCCAAACCTG 312
 529 ArgMetCysCysGluLeuAlaLeuCysLysValValAsnSerHisCysVa 545
 313 CGATGTGCTGTGAGTGGCCCTGTGCAAGGTGGTCAACTCCATGCGT 362
 545 lPheProArgGluLeuLysGluValPheAlaSerTrpArgLeuArgCysA 562
 363 GTTCCCGAGGAGAGCTGAAGAGGTGTTGCGTCCCTGGGACTGCGCTGTG 412
 562 laGluArgGlyArgGluAspIleAlaAspArgLeuIleSerAlaSerLeu 578
 413 CAGAGGGGGCCGAGAGGACATTCGCGACCGGCTGATCAGCCCTCGCTC 462
 579 PheLeuArgPheLeuCysProAlaIleMetSerProSerLeuPhe.GlyL 595
 463 TTCTCGCGTCTCTGCGCGGCCATTATGTCGCCAGCCTNTTCGGGGC 512
 595 euMetGlnGluTyrProAspGluGlnThrSerArgThrLeuLeuIle 611
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 612 Alalys 613
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 clone UUGCIM10164P14 R, DNA sequence.
 ACCESSION AZ399131
 VERSION AZ399131.1 GI:10514203
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 474)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0164 row: P column: 14
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 Location/Qualifiers
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FEATURES
source

/clone_lib="Mouse 10kb plasmid UUGCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 92 a 151 c 131 g 100 t
 ORIGIN

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 Quality: 764.00 Length: 142
 Ratio: 5.380 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.296

alignment_block:
 US-09-294-298-2 x AZ399131/rev ..

Align seg 1/1 to reverse of: AZ399131 from: 1 to: 474
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 255 uAlaArgGluLeuProLysLysArgTyrTyrCysGluLeuCysLeuA 272
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 272 sPaspMetLeuTyrAlaArgThrSerLysProArgSerAlaSerGly 288
 326 ACACATGCTGTATGACCAACCACTCCAAAGCCCGCTCGGCTTCAGGA 277
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 305 lArgAlaLeuArgLeuHisLeuTyrArgAspSerAspLysLysArgLysL 322
 226 CCGGGCCCTTCGGCTGCATCTGTACCGTGACTCAGACAAAAAGCGGAAGA 177
 322 ysAspLysAlaGlyTyrValGlyLeuValThrValProValAlaThrLeu 338
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seq_name: gb_est49:AW779747

Fri Jan 19 06:19:51 2001

seq_documentation_block:	593 bp	mRNA	EST	12-MAY-2000					
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DEFINITION	similar to TR:095174 095174 NGAP. ;, mRNA sequence.								
ACCESSION	AW779747								
VERSION	AW779747.1	GI:7794350							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 593)								
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .							
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index								
JOURNAL	Unpublished (1997)								
CONTACT	Contact: Robert Strausberg, Ph.D.								
	Tel: (301) 496-1550								
	Email: Robert.Strausberg@nih.gov								
COMMENT	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.								
	cDNA Library Preparation: M. Bento Soares, Ph.D.								
	cDNA Library Arrayed by: Greg Lennon, Ph.D.								
	cDNA Sequencing by: Washington University Genome Sequencing Center								
	Clone distribution: NCI-CGAP clone distribution information can be								
	found through the I.M.A.G.E. Consortium/LLNL, send email to:								

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FEATURES
source
    Location/Qualifiers
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           /lab_host="DH10B"
           /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

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BASE COUNT	104 a	169 c	178 g	141 t	1 others
ORIGIN					
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Ratio:	4.143				2
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  US-09-294-298-2  X AW779747/rev  ..
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[illegible]

2008-09-01

100

[illegible][illegible]

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503 CCATCATGATCAGCATCAAGCGCGCTACCAACCATCACCTCCTGCCCAT 454
399 tGluLeuTyrLysGluPheAlaGluTyrValThrAsnHisTyrArgMetL 416
453 GGAGATGTTACAAAGATTCCGTGAGCAGCATCAACCAACCATACCTGTGCGC 404
416 euCysAlaValLeuGluProAlaLeuAsnValLysGlyLysGluGluVal 432
403 TGTGTGCAGCCCTCAGAGCCCATCTCAGTGTGCCACACCAAGGAGGAGTGC 354
433 AlaSerAlaLeuValHisIleLeuGlnSerThrGlyLysAlaLysAspPh 449
353 GCATCTGCCTTGGTGCACATCTCTGAGAGCAGCGGCAAGGTTGAAGGACTT 304
449 eLeuSerAspMetAlaMetSerGluValAspArgPheMetGluAtrGluH 466
303 CTTGTCAGACCTTGATGTTCTCAGAGTGTGACCGCTCGCGGGGCACACGAGC 254
466 isLeuIlePheArgGluAsnThrLeuAlaThrLysAlaIleGluGluTyr 482
253 ACCTCATCTTCGGGGAGAACACACTGGCCACCAAGGCCATTGAGGAGTAC 204
483 MetArgLeuIleGlyGlnLysTyrLeuLysAspAlaIleGlyGluPheI 499
203 CTCAGCTAGTGGCCAGAAAGTACNTGTCAGGAGCGCCCTAGGTGAGTTTCA 154
499 eArgAlaLeuTyrGluSerGluAsnCysGluValAspProIleLysC 516
153 CAAAGCGCTATATGAGTCAGATGAGAACTGCGAAGTGGATGCCAGCAAGT 104
516 yThrAlaSerSerLeuAlaGluHisGlnAlaAsnLeuArgMetCysCys 532
103 GCTCGCGCGTGACCTCCCAGAGCACCAAGGGCAACCTCAAGATGTGCTGC 54
533 GluLeuAlaLeuCysLysValValAsnSerHisCysValPheProArgG 549
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3 3 3

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seq. documentation block: EST 09-FEB-2000
 LOCUS AW421227 597 bp mRNA
 DEFINITION fJ94f10.x1 zebrafish gridded kidney Danio rerio cdna 3' similar to
 TP_005174 095174 NCAP. ; mRNA sequence.

ACCESSION AW421227

VERSION
KEYWORDS
EST.

SOURCE	zebrafish.
ORGANISM	Danio rerio

Eukaryota; Metazoa; Chordata; Vertebrata; Neoptera; Hymenoptera; Ichneumonidae; Braconidae; Eulophinae; Eulophini; Eulophus

Cypriniformes; Cyprinidae

REFERENCE
AUTHORS
Clark, M., Johnson, S. L.

, S.: Hillier, E., Theis
, K.: Steptoe, M., Theis

Swaller, T., Gibbons, M.
Johns, Stephen, Jack

and Wilson, R.

JOURNAL Unpublished (1998)

COMMENT
Other_Esis: 1j24110:1
Contact: Stephen L. Jo

Washington University
4444 Forest Park parkw

Tel: 314 286 1800

Abstract

[REDACTED]